

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claim 1 (currently amended): A nucleic acid enzyme capable of recognizing and cleaving a nucleic acid substrate at a cleavage site which when bound to the substrate comprises:

(a) a substrate binding portion base-paired to [the] 6 nucleotides 3' to the cleavage site of the substrate and which binding portion comprises a six nucleotide sequence wherein its 3'-most first position is a uracil nucleotide and its fourth position is a nucleotide other than a cytosine nucleotide;

(b) a region P3 comprising a double-stranded portion [covalently at a bottom end to the remainder of the ribozyme and capped at a top end by a loop L3] capped at one end by a loop L3 and the first and second strands of which are each bound covalently at another end of the region P3 to one end of the substrate binding portion and to a first strand of one end of region P2 respectively of the enzyme;

(c) the [a] region P2 comprising a double-stranded portion [bound covalently at a bottom end to the remainder of the ribozyme] the first and second strands of which are each bound covalently at the one end to the another end of region P3 and to one end of region J4/2 respectively of the enzyme;

(d) [(f) a single-stranded region, J4/2, covalently bound at one end to the bottom end of P2 and covalently bound at the other end to the bottom end of P4.] the region J4/2 comprising a single-stranded portion bound covalently at the one end to the second strand of the one end of P2 and bound covalently at another end to a first strand of one end of a region P4;

wherein the enzyme is characterized in that

(e) [(d)] the region P4 comprises [comprising] a double-stranded portion [bound covalently at a bottom end to the remainder of the ribozyme, wherein the first base-pair at the bottom end of P4 is a homopurine base-pair] the first and second strands of which are each bound covalently at the one end to the another end of the region J4/2 and to one end of a region

P1.1 respectively of the enzyme, wherein the first base-pair at the one end of region P4 is a homopurine base-pair; and

(f) [(e) a double-stranded region P1.1 formed by base-pairing two nucleotides located between the substrate binding portion and the P4 region, with two nucleotides in the L3 loop; and] the region P1.1 comprises at least two nucleotides base-paired with nucleotides in the loop L3 and the at least two nucleotides are bound covalently at the one end to the one end of P4 and bound covalently at another end to another end of the substrate binding portion.

Claim 2: (now canceled)

Claim 3: (now canceled)

Claim 4 (currently amended): The nucleic acid enzyme according to claim 1, wherein the first base-pair at the another [bottom] end of the region P3 [P3 region] is 3'-U-A-5'.

Claim 5 (currently amended): The nucleic acid enzyme according to claim 1, wherein the double-stranded portion of the region P2 is not capped at another [a top] end.

Claim 6 (currently amended): The nucleic acid enzyme according to claim 5, wherein the first three base-pairs at the another [top] end of the double-stranded portion of the region P2 are each 5'-G-C-3' base-pairs.

Claim 7: (now canceled)

Claim 8 (currently amended): The nucleic acid enzyme according to claim 1, wherein the region P1.1 [stem is comprised] consists of two [GC] base-pairs.

Claim 9: (now canceled)

Claim 10 (currently amended): The nucleic acid enzyme according to claim 1, wherein the region J4/2 [strand is at least] is 5 nucleotides long.

Claim 11 (currently amended): The nucleic acid enzyme according to claim 1, wherein the double-stranded portion of the region P4 [P4 region] comprises the sequence 5'-GCAUGG-3'.

Claim 12 (currently amended): The nucleic acid enzyme according to claim 1, wherein the L3 loop consists of 7 [or fewer] nucleotides.

Claim 13 (currently amended): The nucleic acid enzyme according to claim 1, wherein the nucleic acid enzyme is derived from [antigenomic] hepatitis delta virus.

Claim 14 (previously presented): The nucleic acid enzyme of claim 1, wherein the substrate binding portion of the enzyme additionally comprises a seventh nucleotide attached to the 5'-most end of the six nucleotide sequence.

Claim 15 (previously presented): The nucleic acid enzyme of claim 14, wherein the nucleotide other than a cytosine nucleotide is a nucleotide selected from the group consisting of an adenine nucleotide and a guanine nucleotide.

Claim 16 (previously presented): The nucleic acid enzyme of claim 1, wherein the enzyme is composed of ribonucleotides.

Claim 17 (previously presented): The nucleic acid enzyme of claim 1, wherein the enzyme is composed of a mixture of ribonucleotides and deoxyribonucleotides.

Claims 18 to 30: (now canceled)

Claim 31 (previously presented): A method for cleaving a nucleic acid substrate with a nucleic acid enzyme comprising mixing said substrate with the nucleic acid enzyme of claim 1.

Claim 32 (previously presented): The method of claim 31, wherein the substrate is composed of ribonucleotides.

Claim 33 (previously presented): The method of claim 31, wherein the substrate is composed of a mixture of ribonucleotides and deoxyribonucleotides.

Claim 34 (new): The nucleic acid enzyme according to claim 1, wherein the region P4 is capped at another end by a loop L4 which comprises a sequence selected from the group consisting of 5'-GCUU-3' and 5'-UUCG-3'.

Claim 35 (new): The nucleic acid enzyme according claim 1, wherein said enzyme is a bimolecular enzyme.

Claim 36 (new): The nucleic acid enzyme according to claim 35, wherein said bimolecular enzyme does not comprise an L4 loop.

Claim 37 (new): The nucleic acid enzyme according to claim 1, wherein the homopurine base-pair is GG.

Claim 38 (new): The nucleic acid enzyme according to claim 1, wherein the region P4 has at least five base pairs.

Claim 39 (new): The nucleic acid enzyme according to claim 1, wherein the region P1.1 comprises two GC base pairs, and nucleotide residues at positions -1 and -2 of the substrate directly 5' to the cleavage site do not interact with the two GC base pairs on the region P1.1 of the enzyme.

Claim 40 (new): The nucleic acid enzyme according to claim 1, wherein nucleotide residues of the substrate directly 5' to the cleavage site do not interact with the enzyme.

Claim 41 (new): The nucleic acid enzyme according to claim 1, wherein the nucleotide residue of the substrate directly 3' to the cleavage site is G, forming a GU wobble pair with the enzyme.

Claim 42 (new): The nucleic acid enzyme according to claim 1, wherein the region P1.1 consists of two GC base pairs and the two C residues of the two GC base pairs on the region P1.1 are both on the L3 loop.

Claim 43 (new): The nucleic acid enzyme according to claim 1, wherein the region P1.1 consists of two GC base pairs.